



#2

56

aaagatcaaa ggatcttctt gagatccttt ttttctgcgc gtaatctgct gcttgcaaac 5280
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tccgaaggta actggcttca gcagagcgca gataccaaat actgtccttc tagttagacc 5400
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<210> 17

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer P64-1

<400> 17

tcagcaacca ggctccccag caggc

25

<210> 18

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer 64-4

<400> 18

gacgacagta tcggcctcag gaagatc

27

<210> 19

<211> 840

<212> DNA

<213> Artificial Sequence

<220> Feature

<221> Nucleotide substitutions.

<222> Position 536

<223> At position 536 "n" denotes a or g or c or t/u

<223> Description of Artificial Sequence:

oligonucleotide 80d

<400> 19

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tgtggaaagt cccagggctc ccagcaggc agaagtatgc aaagcatgca tctcaattag 180
tcagcaacca tagtcccgc cctaactccg cccatcccgc ccctaactcc gccagttcc 240
gccattctc cgccccatgg ctgactaatt ttttttatatt atgcagaggc cgaggccgcc 300
tcggcctagg aacagtcgac gacactgcag agacctactt cactaacaac cggtagagtt 360
cgtggaccag atgggtgagg tggagtacgc gcccggggag cccaaagggt accccagttg 420
gggcactact cccgaaaacc gcttctggat ccataacttc gtatagcata cattatacga 480
agttataccg ggccaccatg gtcgcgagta gcttggcact ggggttgctt ttgcgnygtc 540
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ccagctggcg taatagcgaa gaggcccgca ccgatcgccc ttcccaacag ttgcgcagct 660
gaatggcgaa tggcgctttg cctggcttcc ggcaccagaa gcggtgccgg aaagctggct 720
ggagtgcgat cttcctgagg ccgatactgt cgtcaagccg aattctgcag atatccatca 780

Met	Asp	Lys	Leu	Tyr	Cys	Glu	Cys	Gly	Ala	Val	Met	Thr	Ser	Lys	Arg		
370						375					380						
ggg	gaa	gaa	tcg	atc	aag	gac	tct	tac	cgc	tgc	cgt	cgc	cgg	aag	gtg	1200	
Gly	Glu	Glu	Ser	Ile	Lys	Asp	Ser	Tyr	Arg	Cys	Arg	Arg	Arg	Lys	Val		
385					390					395					400		
gtc	gac	ccg	tcc	gca	cct	ggg	cag	cac	gaa	ggc	acg	tgc	aac	gtc	agc	1248	
Val	Asp	Pro	Ser	Ala	Pro	Gly	Gln	His	Glu	Gly	Thr	Cys	Asn	Val	Ser		
				405					410					415			
atg	gcg	gca	ctc	gac	aag	ttc	gtt	gcg	gaa	cgc	atc	ttc	aac	aag	atc	1296	
Met	Ala	Ala	Leu	Asp	Lys	Phe	Val	Ala	Glu	Arg	Ile	Phe	Asn	Lys	Ile		
			420					425					430				
agg	cac	gcc	gaa	ggc	gac	gaa	gag	acg	ttg	gcg	ctt	ctg	tgg	gaa	gcc	1344	
Arg	His	Ala	Glu	Gly	Asp	Glu	Glu	Thr	Leu	Ala	Leu	Leu	Trp	Glu	Ala		
		435					440					445					
gcc	cga	cgc	ttc	ggc	aag	ctc	act	gag	gcg	cct	gag	aag	agc	ggc	gaa	1392	
Ala	Arg	Arg	Phe	Gly	Lys	Leu	Thr	Glu	Ala	Pro	Glu	Lys	Ser	Gly	Glu		
	450					455					460						
cgg	gcg	aac	ctt	gtt	gcg	gag	cgc	gcc	gac	gcc	ctg	aac	gcc	ctt	gaa	1440	
Arg	Ala	Asn	Leu	Val	Ala	Glu	Arg	Ala	Asp	Ala	Leu	Asn	Ala	Leu	Glu		
465					470					475					480		
gag	ctg	tac	gaa	gac	cgc	gcg	gca	ggc	gcg	tac	gac	gga	ccc	gtt	ggc	1488	
Glu	Leu	Tyr	Glu	Asp	Arg	Ala	Ala	Gly	Ala	Tyr	Asp	Gly	Pro	Val	Gly		
				485					490					495			
agg	aag	cac	ttc	cgg	aag	caa	cag	gca	gcg	ctg	acg	ctc	cgg	cag	caa	1536	
Arg	Lys	His	Phe	Arg	Lys	Gln	Gln	Ala	Ala	Leu	Thr	Leu	Arg	Gln	Gln		
			500					505					510				
ggg	gcg	gaa	gag	cgg	ctt	gcc	gaa	ctt	gaa	gcc	gcc	gaa	gcc	ccg	aag	1584	
Gly	Ala	Glu	Glu	Arg	Leu	Ala	Glu	Leu	Glu	Ala	Ala	Glu	Ala	Pro	Lys		
		515				520						525					
ctt	ccc	ctt	gac	caa	tgg	ttc	ccc	gaa	gac	gcc	gac	gct	gac	ccg	acc	1632	
Leu	Pro	Leu	Asp	Gln	Trp	Phe	Pro	Glu	Asp	Ala	Asp	Ala	Asp	Pro	Thr		
	530					535					540						
ggc	cct	aag	tcg	tgg	tgg	ggg	cgc	gcg	tca	gta	gac	gac	aag	cgc	gtg	1680	
Gly	Pro	Lys	Ser	Trp	Gly	Arg	Ala	Ser	Val	Asp	Asp	Lys	Arg	Val			
545				550					555					560			
ttc	gtc	ggg	ctc	ttc	gta	gac	aag	atc	gtt	gtc	acg	aag	tcg	act	acg	1728	
Phe	Val	Gly	Leu	Phe	Val	Asp	Lys	Ile	Val	Val	Thr	Lys	Ser	Thr	Thr		
				565					570					575			
ggc	agg	ggg	cag	gga	acg	ccc	atc	gag	aag	cgc	gct	tcg	atc	acg	tgg	1776	
Gly	Arg	Gly	Gln	Gly	Thr	Pro	Ile	Glu	Lys	Arg	Ala	Ser	Ile	Thr	Trp		
			580					585					590				
gcg	aag	ccg	ccg	acc	gac	gac	gac	gaa	gac	gac	gcc	cag	gac	ggc	acg	1824	
Ala	Lys	Pro	Pro	Thr	Asp	Asp	Asp	Glu	Asp	Asp	Ala	Gln	Asp	Gly	Thr		
		595					600					605					
gaa	gac	gta	gcg	gcg	cct	aag	aag	aag	agg	aag	gtt	tag				1863	
Glu	Asp	Val	Ala	Ala	Pro	Lys	Lys	Lys	Arg	Lys	Val						
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<210> 23

<211> 620

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence
encoding the fusion protein C31-Int(CNLS)

<400> 23

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Asp	Arg	Gln	Ser	Arg	Glu	Arg	Glu	Asn	Ser	Ser	Ala	Ala	Ser	Pro	Ala	20	25	30	
Thr	Gln	Arg	Ser	Ala	Asn	Glu	Asp	Lys	Ala	Ala	Asp	Leu	Gln	Arg	Glu	35	40	45	
Val	Glu	Arg	Asp	Gly	Gly	Arg	Phe	Arg	Phe	Val	Gly	His	Phe	Ser	Glu	50	55	60	
Ala	Pro	Gly	Thr	Ser	Ala	Phe	Gly	Thr	Ala	Glu	Arg	Pro	Glu	Phe	Glu	65	70	75	80
Arg	Ile	Leu	Asn	Glu	Cys	Arg	Ala	Gly	Arg	Leu	Asn	Met	Ile	Ile	Val	85	90	95	
Tyr	Asp	Val	Ser	Arg	Phe	Ser	Arg	Leu	Lys	Val	Met	Asp	Ala	Ile	Pro	100	105	110	
Ile	Val	Ser	Glu	Leu	Leu	Ala	Leu	Gly	Val	Thr	Ile	Val	Ser	Thr	Gln	115	120	125	
Glu	Gly	Val	Phe	Arg	Gln	Gly	Asn	Val	Met	Asp	Leu	Ile	His	Leu	Ile	130	135	140	
Met	Arg	Leu	Asp	Ala	Ser	His	Lys	Glu	Ser	Ser	Leu	Lys	Ser	Ala	Lys	145	150	155	160
Ile	Leu	Asp	Thr	Lys	Asn	Leu	Gln	Arg	Glu	Leu	Gly	Gly	Tyr	Val	Gly	165	170	175	
Gly	Lys	Ala	Pro	Tyr	Gly	Phe	Glu	Leu	Val	Ser	Glu	Thr	Lys	Glu	Ile	180	185	190	
Thr	Arg	Asn	Gly	Arg	Met	Val	Asn	Val	Val	Ile	Asn	Lys	Leu	Ala	His	195	200	205	
Ser	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Phe	Glu	Phe	Glu	Pro	Asp	Val	Ile	210	215	220	
Arg	Trp	Trp	Trp	Arg	Glu	Ile	Lys	Thr	His	Lys	His	Leu	Pro	Phe	Lys	225	230	235	240
Pro	Gly	Ser	Gln	Ala	Ala	Ile	His	Pro	Gly	Ser	Ile	Thr	Gly	Leu	Cys	245	250	255	
Lys	Arg	Met	Asp	Ala	Asp	Ala	Val	Pro	Thr	Arg	Gly	Glu	Thr	Ile	Gly	260	265	270	
Lys	Lys	Thr	Ala	Ser	Ser	Ala	Trp	Asp	Pro	Ala	Thr	Val	Met	Arg	Ile	275	280	285	
Leu	Arg	Asp	Pro	Arg	Ile	Ala	Gly	Phe	Ala	Ala	Glu	Val	Ile	Tyr	Lys	290	295	300	
Lys	Lys	Pro	Asp	Gly	Thr	Pro	Thr	Thr	Lys	Ile	Glu	Gly	Tyr	Arg	Ile	305	310	315	320
Gln	Arg	Asp	Pro	Ile	Thr	Leu	Arg	Pro	Val	Glu	Leu	Asp	Cys	Gly	Pro	325	330	335	